

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: JACOBSON, Myron K.; JACOBSON, Elaine L.; AMÉ, Jean-Christophe; LIN, Winston

(ii) TITLE OF INVENTION: GENES ENCODING SEVERAL POLY(ADP-RIBOSE) GLYCOHYDROLASE (PARG) ENZYMES, THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIVE THEREWITH

(iii) NUMBER OF SEQUENCES: 38

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Fulbright & Jaworski L.L.P.  
(B) STREET: 666 Fifth Avenue  
(C) CITY: New York  
(D) STATE: New York  
(E) COUNTRY: USA  
(F) ZIP: 10103

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
(B) COMPUTER: IBM PS/2  
(C) OPERATING SYSTEM: PC-DOS  
(D) SOFTWARE: Wordperfect

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned  
(B) FILING DATE: Concurrently Herewith

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: John E. Lynch  
(B) REGISTRATION NUMBER: 20,940  
(C) REFERENCE/DOCKET NUMBER: NIAD 201-JEL/ES

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 212-318-3000  
(B) TELEFAX: 212-752-5958

05973451 100904

(2) INFORMATION FOR SEQ ID NO: 1:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 4069 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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1  acccgaaagt  gaacgaagcc  cgaatcagaa  cggctcatcc  tgaggctggt  aggggtgccg
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121  ctgcagaagc  agtcagcggc  agagggggca  tgggtgccgg  aggcaccgag  gagggggcgc
181  agtccgtccc  tcccagggtt  agtgaatgag  gctctacgcc  cgggctggcc  cggagactca
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301  gctgggacgc  cgctgcaact  tctccgcggg  ccgcctcgga  cgcccgagc  ttccccggca
361  ggcagaggcg  cgctcctgat  tccaaggacg  ctccggtgca  gttcagggtc  ccgccgtcct
421  cgtcaggctg  cgccctgggc  cgggcgggac  agcaccgagg  cagcgccacc  tctcttggtt
481  tcaaacagaa  gactataacc  agttggatgg  aactaaagg  aatcaagaca  gttgaatcag
541  aaagtttgca  tagtaaagaa  aacaacaata  caagagaaga  atccatgatg  agttctgtac
601  aaaaagataa  cttttatcaa  cataacatgg  aaaaattaga  aaatgtttct  cagctaggtt
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841  atgatcacag  tgacacaaat  agtgaggaga  gtagagataa  tcagcagttt  ttgacacatg
901  taaagcttgc  gaatgcaaag  cagacgatgg  aagatgaaca  gggcagagaa  gccagaagcc
961  accagaagtg  tggcaaggct  tgccatcctg  cagaagcctg  tgcagggtgt  cagcaggagg
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1501  tcattgagtg  gcccaaagca  gaggacaaaa  gaaaagaaca  atgtgaaatg  aaacatcaaa
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1621  ttggaactcc  tattgaggag  atgaggagaa  tgccaagggt  tgggatccgg  ctgcctccct
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1981  ttgattttct  ggataaggta  ctagaagaag  cagaagctca  acacttgat  cagtccatct
2041  tgccctgat  ggtgaaaatt  gcactctgtc  tgccaaatat  ttgtaccag  ccaataccac
2101  tcctgaaaca  gaagatgaat  cattccatca  caatgtcaca  ggaacagatt  gccagtcttt
2161  tagctaattg  tttcttctgc  acgtttccac  gacgcaatgc  caagatgaaa  tcagagtatt
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2461  tacagggtgga  ttttgcaaac  cgtttcgttg  gaggtggtgt  aaccagtgc  ggacttggtc
2521  aagaagaaat  ccgcttttta  atcaaccctg  agttgattgt  ttcacggctc  ttcactgagg
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09973451.100501

3121 cattcatata ccatgcagtt gagtcctgta cacagaccac caaccagccg ggacaaaagga  
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 3241 gtgtgaactg acatgatata catgtgtata taatccgcgt ttgtaggcaa ggatgcagtc  
 3301 ccttccgccc atgcagctgt cagtacatct gcgcctcctc catcccgact tacatagact  
 3361 gagacatact ttgtttcttt ttttttctat ttcagccctg attcttttat ttttctttct  
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 3481 ttttttgatg cctaaatata caaatcacct ctgcagctag cagatgccac ggaaggtggt  
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 3601 ccctattatc attgtggtgg tggaggtttt ttgatttttg aaataagagt tgggtttggt  
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 3781 ttgtattgac tgtttttgga aattgaccca aatgaaagga aatatgagaa taagagtttc  
 3841 ccaaattggtg tttaaaaaca aacagggttca agacacgcga aggacctcgt ttcctgggat  
 3901 tttttttctt tttctttttt tgaattagga ttattgtttg ttccttggtg cttgagacat  
 3961 attcatataa ccaaagttaa ggaactggga acttcgtggt gatttgtaca tattgaagtt  
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(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 977 amino acids
- (B) TYPE: protein
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

1 MSAGPGCEPC TKRPRWDAAA TSPPAASDAR SFPGRQRRVL DSKDAPVQFR VPPSSSGCAL  
 61 GRAGQHRGSA TSLVFKQKTI TSWMDTKGIK TVESESLHSK ENNNTREESM MSSVQKDNFY  
 121 QHNMEKLENV SQLGFDKSPV EKGTOYLKQH QTAAMCKWQN EGPHSERLLE SEPPAVTLVP  
 181 EQFSNANVDQ SSPKDDHSDT NSEESRDNDQ FLTHVKLANA KQTMEDDEQGR EARSHQKCGK  
 241 ACHPAEACAG CQQEETDVVS ESPLSDTGSE DVGTGLKNAN RLNRQESSLG NSPPFEKESE  
 301 PESPMVDVNS KNSCQDSEAD EETSPGFDEQ EDSSSAQTAN KPSRFQPREA DTELKRSSA  
 361 KGGEIRLHFQ FEGGESRAGM NDVNAKRPGS TSSLNVECRN SKQHGRKDSK ITDHFMRVPK  
 421 AEDKRKEQCE MKHQRTTERKI PKYIPPHLSP DKKWLGTPIE EMRRMPRCGI RLPPLRPSAN  
 481 HTVTIRVDLL RIGEVPKPFP THFKDLWDNK HVKMPCSEQN LYPVEDENGE RAAGSRWELI  
 541 QTALLNRLTR PQNLKDAILK YNVAYSKKWD FTALIDFWDK VLEEAEAAQHL YQSILPDMVK  
 601 IALCLPNICT QPIPLLKQKM NHSITMSQEQ IASLLANAFF CTFFRRNAKM KSEYSSYPDI  
 661 NFNRLFEGRS SRKPEKLKTL FCYFRRVTEK KPTGLVTFTR QSLDFPEWE RCEKLLRLH  
 721 VTYEGTIEGN GQGMLOVDFA NRVVGGGVTs AGLVQEEIRF LINPELIVSR LFTEVLHDNE  
 781 CLITGTGEQY SEYTYAETY RWARSHEDRS ERDDWQRRTT EIVADALHF RRYLDQFVPE  
 841 KIRRELNKAY CGFLRPGVSS ENLSAVATGN WCGAFGGDA RLKALIQILA AAVAERDVVY  
 901 FTFGDSELMR DIYSMHTFLT ERKLTVEGEV KLLRLYYNEE CRNCSTPGPD IKLYPFIYHA  
 961 VESCTQTTNQ PGQRTGA

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4069 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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 61 gggccaaggc aggcgctgag aaggacgcgc agtccatctc tctcagggtta gtgaaatgag  
 121 gctctccgcg gggccggccc ggggacagtg cgctgctggt cccagcatga atgcgggccc  
 181 cggctgtgaa ccctgcacca aagcgacccg ctggggcgcc gctacaactt cgccggctgc  
 241 ttcggacgcc cggagctttc cgagcaggca gaggcgcgct ctcgacccca aggacgctca  
 301 cgtgcagttc aggggtccac cgtcctcgcc agcctgcgct ccagggcagg cgggacagca

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361 cagagggcagc gccacctcgc ttgtttttcaa acaaaagact attaccagtt ggatggacac
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481 aatagaatcc atgatgagtt ctgtacaaaa agataacttt taccaacata atgtagaaaa
541 attagtaaat gtttctcagc taagtcttga taagtcactc actgaaaaaa gtacacagta
601 tttgaaccag catcagactg cagcaatgtg taagtggcaa aatgaaggga aacacacgga
661 gcagcttttg gaaagtgaac ctcaaacagt aaccctggta ccagagcagt ttagtaatgc
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1861 taagaaatgg gactttacag ccattcttgc tgatatggtg aaaattgcac tctgtctgcc
1921 agctcaacat acccagccaa taccactcct gaaacagaag atgaatcatt ccatcacaat
1981 aaatatttgc gactttgcca gtcttttagc taatgctttc ttctgcacat tccacgcagc
2041 gtcgcaggaa atgaaatcgg agtattctag ttaccagac attaaacttca atcgattggt
2101 aaatgctaa gtcattcaagg aaccggagaa acttaaaacg ctcttctgct actttagaag
2161 tgaggggacgt tcatcaagga ctgggttggg gacatttaca agacagagtc ttgaagattt
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2281 tccagaatgg gaaagatgtg gcatgtcaca ggtggatttt gcaaatcggt ttgttggagg
2341 catagaagaa aatggccaag agtgcaggac ttgtgcaaga agaaatccgc tttttaatca atcctgagtt
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3061 aagttaatat aaatgtgtac ataattccaca tttgtagtca aggacgcaat gctaataatc
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3181 atatgttttg tttctatttt ctctattttc agtttttcat tctttgatgt ttatttcttt
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3301 ctctcctgcc atatatata ccagttgctt ctgcagcccg cagatgccc aagccttga
3361 ggaaacaagt tgaaatccca ggaactctct taactgattt tgctaaaaat ctccctgtga
3421 gccttccact caactcttaa tatgcttgca ttgtttaagt ttttaaattc tgaaaaattaa
3481 taattagggg ttttttcata tgtgttgcac aatgcaaaac tcctaggtta aaatagtttc
3541 tttatttaag atagaataat ttccagaaat tgtacttttg aggtatcatt tttatctgta
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3721 gattccaaga gaattgaaga ttttttttgt ttcttgggta cttttttctt tttaaattag
3781 gaacttcatt tcttttggg catattgaag tttctctggt attcaaaggt tatatagtga
3841 atgaattttc attaataaat cactttgtca gaaaaaaaaa aaaaaaaa

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- (2) INFORMATION FOR SEQ ID NO: 4:  
 (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 976 amino acids  
     (B) TYPE: protein  
     (C) STRANDEDNESS: single  
     (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

1	MNAGPGCEPC	TKATRWGAAT	TSPAASDARS	FPSRQRRVLD	PKDAHVQFRV	PPSSPACVPG
61	QAGQHRGSAT	SLVFKQKTIT	SWMDTKGIKT	AESESLDSKE	NNNTRIESMM	SSVQKDNFYQ
121	HNVEKLVNVS	QLSLDKSLTE	KSTQYLNQHQ	TAAMCKWQNE	GKHTEQLLS	EPQTVTLVPE
181	QFSNANIDRS	PQNDDHSDTD	SEENRDNQQF	LTTVKLANAK	QTTEDEHARE	AKSHQKCSKS
241	CHPGEDCASC	QQDEIDVVPK	SPLSDVGSSE	VGTGSKNDNK	LIRQESCLGN	SPPFEKESEP
301	ESPMVDVNSK	NSCQDSEADE	ETSPGFDEQE	DGSSSQDTANK	PSRFQARDAD	IEFRKRYSTK
361	GGEVRLHFQF	EGGESRTGMN	DLNAKLPGNI	SSLNVECRNS	KQHGKKDSKI	TDHLMRLPKA
421	EDRRKEQWET	KHQRTERKIP	KYVPPHLSPD	KKWLGTPIEE	MRRMPRCGIR	LPLLRPSANH
481	TVTIRVDLLR	AGEVPKPFPT	HYKDLWDNKH	VKMPCSEQNL	YPVEDENGER	TAGSRWELIQ
541	TALLNKFTRP	QNLKDAILKY	NVAYSKKWDF	TALIDFWDKV	LEEAEAOHLY	QSILPDMVKI
601	ALCLPNICTQ	PIPLLKQKMN	HSITMSQEQI	ASLLANAFFC	TFPRRNAKMK	SEYSSYPDIN
661	FNRLFEGRSS	RKPEKLKTLF	CYFRRVTEKK	PTGLVTFTRO	SLEDFPEWER	CEKPLTRLHV
721	TYEGTIEENG	QGMQLQVDFAN	RFVGGGVTS	GLVQEEIRFL	INPELIISRL	FTEVLHDNEC
781	LIITGTEQYS	EYTGAAETYS	WSRSHEDGSE	RDDCERRCTE	IVAIIDALHFR	RYLDQFVPEK
841	MRRELNKAYC	GFLRPGVSSE	NLSAVATGNW	GCGAFGGDAR	LKALIQILAA	AAAERDVVYF
901	TFGDSELMRD	IYSMHIFLTE	RKLTVGDVYK	LLRYYNEEC	RNCSTPGPDI	KLYPFIYHAV
961	ESCAETADHS	GQRTGT				

- (2) INFORMATION FOR SEQ ID NO: 5:  
 (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 3814 base pairs  
     (B) TYPE: nucleic acid  
     (C) STRANDEDNESS: single  
     (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

1	gggggactgt	gtgctgcggg	tcccagcatg	agtgcggggc	ccggtcggga	gccctgcacg
61	aaagcgcgct	ggggcgccgc	tggaacttct	gcgcgcactg	cctcgactc	ccggagcttc
121	cctggcagcg	agaggcgtgt	tctcgacccc	aaggacgctc	ccgtccagtt	cagggtccct
181	ccgtcctcgc	cagcctgcgt	ctcggggcgg	gcgggaccgc	acagaggcaa	cgccacctcg
241	tttgttttca	aacaaaagac	tattactact	tggatggata	ctaaaggacc	caagacagct
301	gaatcagaaa	gtaaaagaaa	caacaatata	agaattgact	ccatgatgag	ttctgtgcag
361	aaagataact	tttaccacaa	taaggtggaa	aaattggaaa	atgttcctca	gctaaatctt
421	gataaatcac	ccacagaaaa	gagttcacag	tatttgaacc	aacagcagac	tgcgagtgtg
481	tgcaagtggc	agaatgaagg	gaagcatgca	gaacagcttt	tggcaagtga	gcctcccgcg
541	gggactccgc	taccaaagca	gcttagtaat	gctaacattg	gtcagtcacc	ccacactgat
601	gaccacagtg	acacagatca	tgaagaagac	agagacaatc	agcagtttct	tacacctata
661	aaacttgcaa	atacaaagcc	aacagtagga	gatgggcagg	ccagaagcaa	ctgtaagtgc
721	agtggatctc	gccagtctgt	gaaagactgt	acaggctgtc	aacaggaggga	ggtggatgtg
781	ctaccagaga	gtcctttgtc	agatgttggt	gccgaggaca	ttggaactgg	accaaaaaat
841	gacaacaaat	tgactggaca	agaaagcagc	ctaggtgatt	cgctccatt	tgagaaagaa
901	agtgagcctg	agtcaccaat	ggatgtagac	aactcgagaa	acagttgtca	agattcagaa
961	gcagatgaag	aaacaagtcc	agtctttgat	gagcaagatg	atcgttcctc	ccaaacagca
1021	aataaacttt	caagttgcca	agcaagagaa	gctgatggcg	atcttaggaa	acggtatttg
1081	actaagggaa	gtgaagttag	attgcatttc	caatttgaag	gagaaaaata	tgctgggacc
1141	agtgacttaa	atgccaaagc	atctggaaac	tcttctagcc	ttaatgtaga	gtgtagaagt
1201	tccaagcagc	atggaaaaag	gattctctaa	attacagatc	atttcattag	aatttccaag
1261	tcagaggaca	gaagaaaaga	acaatgtgaa	gtcagacatc	aaagaacaga	aaggaagatt
1321	ccaaaataca	tcccacctaa	cctccctcca	gagaagaagt	ggctgggaac	tcctattgag

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1381 gaaatgagaa aaatgcctcg gtgtgggacg catttgcctt ccttaagacc atctgcaagt
1441 cacacagtga ctgttcgggt agaccttctg agagcaggag aggttccgaa accttttcca
1501 acacattaca aagattttgtg ggataacaaa catgtgaaaa tgccttggtc ggaacaaaac
1561 ttgtacctcg tggaagatga gaatggtgag cgaactgcag ggagtaggtg ggagctcatt
1621 cagactgcac ttctcaacaa attcacacga cccagaact tgaaggatgc gattctgaaa
1681 tacaatgtgg catattctaa gaaatgggac tttacagctt tgggtgattt ctgggataag
1741 gtacttgaag aagcagaggc ccaacattta tatcagtcca tttacctga catggtgaaa
1801 attgcactct gtctgccaaa tatttgcacc cagccaatac cactcctgaa acagaagatg
1861 aatcattctg tcacgatgtc acaggaacag atcgccagtc ttttagctaa tgctttcttc
1921 tgcacatttc cccgacggaa tgccaagatg aaatcggagt attctagtta cccagacatt
1981 aacttcaate gggtgtttga aggacgttca tcaaggaaac cagaaaaact cagaaacactc
2041 ttctgtctact ttgcaagagt cacagagaaa aaacctacag gattggtgac atttacaaga
2101 cagagtcttg aagattttcc agaatgggaa aggtgtgaaa agcctctgac acgcttacac
2161 gtcacttacg agggtagcat agaaggcaac ggccgaggca tgctacaggt ggattttgca
2221 aatcggtttg ttggaggtgg tgtgactggt gcgggacttg tacaagaaga aatcagattt
2281 ttaatcaatc ctgaattgat tgtttcacgg ctgttactg aggtgctgga tcacaatgag
2341 tgtcttatta tcacaggtac tgaacagtac agtgaatata caggctatgc tgaaacttat
2401 cgttgggccc gaagccatga agatgggagt gaaaaggacg attggcagcg gcgctgcacg
2461 gagatcggtg ccattgacgc acttcaactc agacgctacc tcgatcagtt tgtgcctgag
2521 aaagtgagac gtgagcttaa caaggcttac tgcggattcc tccgtcctgg agttccttct
2581 gaaaatcttt ctgcagtggc cacgggaaac tggggctgtg gtgccttttg ggtgacgct
2641 agattaaaaa ccttaataca gatcctggga gctgctgcgg ctgaacgtga cgtggtttat
2701 ttacaccttg gggactcaga gttgtagaga gacatttata gcatgcacac tttccttacc
2761 gagaggaagc tggatgttgg aaaagtgtac aagttattgc ttagatacta caatgaagaa
2821 tgcagaaact gttccacccc tggaccagac atcaagcttt atccattcat ataccatgct
2881 gttgagtcaa gtgcagagac cactgacatg ccaggacaga aggcaggcac ctgaggaaca
2941 agtgactagg acctcctctc aaagagacat cctatttgaa atgtgggggtg tgatgtctga
3001 attgactgaa tctgatctaa gtgtgtatat aatccacatt tgtaatcaag gatgcagtct
3061 cttctgcata tgcagttggt tcttgttcat cctggtggac atgcctttag acatggcttc
3121 ttcaattttt ctctccttc agtctttatt ctttgatttt ttttttccaa cttgatttct
3181 tgggaaaaact caagaaaggt tgcactcagc ttctagatct ttctcttcct gtctgtgtgt
3241 tgtccagact gctttggtgg ctagcagata ccacacact tggaggaagt taaaaatcca
3301 gaaatctgag tttgctgcag atttacctgt gagcttctca ctcccaaccc ttgttaggct
3361 tgtgttgtct acattttcaa ttttggaagt tgaagttttt cttatgttac ttaatgctag
3421 tatcttttag gctaaaaacta ttttctattt aaggcagact aatttccagt ttctcttttg
3481 aaacatcatc cctataagta acggtttttt tgcctctttt tccccagcg ctattttaga
3541 agctggccaa gaggaagaa aatgtagaat aaaaggattt tcctcggatg ctataaagaa
3601 gccaggttca agagcgttgg ggtttttgtt tttttcaaga cttgtttttc ctttgagct
3661 agggtagtg cttgttctgt ggtgctgagg gcatagtcct gtaaccaaag gtctttgctg
3721 gagacttgat gctgatttgt acatatggaa gtttctctgg caggaaatat tagagttaat
3781 aaatttcatt aataaatcat ttgtcagaaa aaaa

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(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 968 amino acids
- (B) TYPE: protein
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```

1   MSAGPGWEPK TKARWGAAGT SAPTASDSRS FPGRQRRVLD PKDAPVQFRV PPSSPACVSG
61  RAGPHRGNAT SFVFKQKTIT TWMDTKGPKT AESESKENNN TRIDSMSSV QKDNFYPHKV
121 EKLENVPLQN LDKSPTEKSS QYLNQQQTAS VCKWQNEGKH AEQLLASEPP AGTPLPKQLS
181 NANIGQSPHT DDHSDTDHEE DRDNQQFLTP IKLANTKPTV GDGQARSNCK CSGSRQSVKD
241 CTGCQQEEVD VLPESPLSDV GAEDDGTGPK NDNKLTGQES SLGDSPPFEK ESEPESPM DV
301 DNSRNSCQDS EADEETSPVF DEQDDRSSQT ANKLSSCQAR EADGDLRKRY LTKGSEVRLH
361 FQFEGENNAG TSDLNAKPSG NSSSLNVECR SSKQH GKRDs KITDHFMRIS KSEDRRKEQC
421 EVRHQRTERK IPKYIPP NLP PEKKWLGTPI EEMRKMPRCG IHLPSLRPSA SHTVTVRVDL
481 LRAGEVPKPF PTHYKDLWDN KHKVMP CSEQ NLYPVEDENG ERTAGSRWEL IQTALLNKFT

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541 RPQNLKDAIL KYNVAYSKKW DFTALVDFWD KVLEEEAEQHQ LYQSILPDMV KIALCLPNIC  
601 TQPIPLLKQK MNHSTVMSQE QIASLLANAF FCTFPRRNAK MKSEYSSYPD INFNRLFEGR  
661 SSRKPEKLKT LFCYFRRVTE KKPTGLVTFT RQSLDFPEW ERCEKPLTRL HVTYEGTIEG  
721 NGRGMLQVDF ANRFVGGVT GAGLVQEEIR FLINPELIVS RLFTEVLHDN ECLIITGTEQ  
781 YSEYTGAAET YRWARSHEDG SEKDDWQRRR TEIVAIDALH FRRYLDQFVP EKVRRELNKA  
841 YCGFLRPGVP SENLSAVATG NWGCGAFGGD ARLKALIQIL AAAAAERDVG YFTFGDSELM  
901 RDIYSMHTFL TERKLDVGKV YKLLLLRYNE ECRNCSTPGP DIKLYPFIYH AVESSAETTD  
961 MPGQKAGT

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2781 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

1 tcgaagtgtg tggatattat aaagtgcgat attcatcaca gctatcgctc atccccaaaa  
61 caccgggtatg caagaattca ggtcacactt gattttttccg atattccaaa aggtttacca  
121 atctacggca aatcgccgca gagcaagtgc atccgtgctg accaatcgac tcggcaaggc  
181 tttgtgctta aactgcgcca ggatgtcgaa gtcgcccgat ggccgggattt ccgaaataga  
241 aacggaggag gagccgaaa atctggcgaa ctccctagat gattcgtggc gtggagtttc  
301 catggaggct atacatcgta atcggcagcc ttctgaattg gagaatttgc caccagtgc  
361 tgccggcaat ctccaccggg ttatgtacca gctgccaatt cgtgaaacac cgccacgccc  
421 ctacaaatca ccgggaaagt gggactccga gcatgtgcgt ctgccctgtg cgcccgagtc  
481 gaaatatccg agggagaatc cggatggcag caccaccatc gatttttcgt gggaatgat  
541 cgaacgagcc cttctgcagc ccataaagac gtgtgaggaa ctgcaggcgg cgataatatc  
601 atataatacc acctataggg atcagtggca ctttctgtgc cttcatcaac ttctcgacga  
661 ggaactggac gagagcgaaa cacgggtttt cttcgaggat ctattgccgc gcattatccg  
721 attggcattg cggctaccgg acttgattca atcgccagtt ccgctgctca agcaccacaa  
781 gaacgcctca ttgagcctga gccaacagca gatctcctgc ctgttgcca atgccttctt  
841 gtgcacgttt ccccgaaaga acacctcaa gaggaagtcc gactacagca cttttccaga  
901 catcaacttt aacaggcttt accaatcgac gggaccggca gttctggaga agcttaaatg  
961 cattatgcac tattttcgtc gcgtgtgtcc cacagagcgg gatgccagca atgtgcccac  
1021 cgggtgtgta acctttgttc gtcggagcgg attgccggaa catctgatcg actggagcca  
1081 aagtgcggcg ccgttgggtg atgtgccatt gcacgtggat gccgagggaa caatcgagga  
1141 tgagggcatt ggactgctgc aagtagactt tgccaacaaa tatttgggtg gcggtgtctt  
1201 gggactatgg tcgcttcagg agggagatac ctttgttatc tgtccggagc ttttccagg  
1261 taaactcttt acggagtgtc tgcgaccatt cgaggccctg gtgatgttgg gcgccgaaag  
1321 gtatagtaac tatacgggat atgccggaag cttcgagtgg tccggcaact ttgaggattc  
1381 aacgccaaga gatagctcag gtcgtcgaca aacggccatt gtggcaatcg atgccctaca  
1441 ttttgcccag tcacatcatc aatatcgcca ggatctcatg gaaagggagc tgaacaaggc  
1501 gtacattgga tttgttcaat ggatggtgac gccgccaccg ggtgtggcaa ctggttaactg  
1561 ggggttgccg gcattcggcg gtgactccta tctgaaagcc ctgctgcaac ttatggtctg  
1621 cgcccagttg ggcagacctt tggcctacta tacctttgga aatgtggagt ttagggatga  
1681 ttttcatgaa atgtggctgt tgtttcgaaa tgacgggact acggtgcagc agctttggag  
1741 tatttttaagg tcgtacagta ggcttattaa ggagaagagc tccaaggagc cgcgtgagaa  
1801 taaggcatcc aaaaagaagc tatatgattt tattaaagag gaacttaaga aggtcagaga  
1861 tgtgcccgga gagggagcat ccgccgaagc tggaagctct agagtagctg gattaggcga  
1921 aggaaaaatca gaaacatcag cgaatccctc gccagaactc aacaagcaac ccgccgacc  
1981 gcaaatcacc ataacgcaac aaagtaaccg tctattgccc gcgcaattat cgcaagataa  
2041 ctctaattct tcggaagatc aggccttctt tatgctgtcg gacgatgagg aggccaatgc  
2101 catgatggag gccgctagtc tggaggctaa aagcagcgta gaaataagca acagcagcac  
2161 aacgtccaaa acgagcagta cagccacgaa atcaatgggt tcagggtggc gccagttgag  
2221 tctgctcgag atgctggaca ccattatga aaagggttcg gcctcgaaga ggccacgaaa  
2281 atcacccaac tgcagcaagg ctgagggttc agcaaagagt cgttaaggaga tcgatgtgac  
2341 cgacaaggac gaaaaggacg atattgttga ctaggtgata ttgcactaca ggattgttac  
2401 tgcccccaaa aattgaagag gtataaaatg tattgtagat aactttaagg acatatttag  
2461 ggcatttttaa agtaggatca ttgtaagtcg aataaagtga aatttttttt tttttttaat

2521 tatactattc taatctgcaa agacaatttt actgttaaatt ttgtataaca ttcgaattaa  
 2581 ttaatataat ttgttatatc atgcaaattc agcttttatt atgcgaaatt tgtagttaaa  
 2641 gccagtaaag tttcttttta ttttaaccgaa accttttggt tattttattt gaccacaaca  
 2701 agaacatcaa caacaacaac cacgaaaaaa aagcgaatat atatttggtt gttcgtatat  
 2761 atatatatat ctaagcagat c

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 768 amino acids
- (B) TYPE: protein
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

1 MQEFRSHLIF PIFQKVYQST ANRRRASASV LTNRLGKALC LNCARMSKSP DGGISEIETE  
 61 EEPENLANSL DDSWRGVSM EAIHRNRQPF LENLPPVTAG NLHRVMYQLP IRETPPRPYK  
 121 SPGKWDSEHV RLPCAPESKY PRENPDGST IDFRWEMIER ALLQPIKTCE ELQAAIISYN  
 181 TTYRDQWHFR ALHQLLDEEL DESETRVFFE DLLPRIIRLA LRLPDLIQSP VPLLKHHKNA  
 241 SLSLSQQQIS CLLANAFCT FPRNTLKRK SEYSTFPDIN FNRLYQSTGP AVLEKLCIM  
 301 HYFRRVCPE RDASNVTGV VTFVRRSGLP EHLIDWSQSA APLGDVPLHV DAEGTIEDEG  
 361 IGLLQVDFAN KYLGGGVVLGH GCVQEEIRFV ICPELLVGLK FTECLRPFEA LVMLGAERY  
 421 NYTGYAGSFE WSGNFEDSTP RDSSGRRQTA IVAIDALHFA QSHHQYREDL MERELNKAYI  
 481 GFVHWMVTPP PGVATGNWGC GAFGGDSYLK ALLQLMVCAQ LGRPLAYYTF GNVEFRDDFH  
 541 EMWLLFRNDG TTVQQLWSIL RSYRLIKEK SSKEPRENKA SKKKLYDFIK EELKKVRDVP  
 601 GEGASAEAGS SRVAGLGEGK SETSAKSSPE LNKQPARPQI TITQQSTDLL PAQLSQDNSN  
 661 SSEDQALLML SDDEEANAMM EAASLEAKSS VEISNSSTTS KTSSTATKSM GSGGRQLSLL  
 721 EMLDTHYEKG SASKRPRKSP NCSKAEGSAK SRKEIDVTDK DEKDDIVD

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

1 ATGAGCAAGA AGTTTATCGA ACTGGGTGAT CCTGTCACTC AAGACGAGAA  
 51 AGACTACGAA GACTATGTCG GAGTTGGTTT CGCGCATCAA GTCCCCGACAA  
 101 TGAAAAGGCG GAAGTTGACA GAACATGGAA ATACTACAGA ATCAAAAAGAA  
 151 GATCCTGAAG AGCCAAAAAG CCGTGACGTA TTTGTCTCCT CGCAGTCAAG  
 201 TGATGAGAGT CAAGAAGATT CGGCTGAAAA TCCGGAGATC GCTAAAGAAG  
 251 TGTCAGAAAA TTGTGAAAT CTGACAGAAA CTCTCAAAAT TTCTAATATT  
 301 GAGAGTTTGG ACAATGTTAC TGAAAGATCT GAACACACTC TTGATAATCA  
 351 CAAAAGTACT GAACCAATGG AAGAAGATGT AAACAACAAG TCCAATATTG  
 401 ACGTTGCGAT TAATTCTGAC GAGGATGATG AACTTGTTCT GGAAGAGAAT  
 451 AATAAAGAAA TGAGGGATGG AGAACAAGTA CAACAGTTGT CACAGGATTT  
 501 ATTCGCTGAT GATCAAGAGC TAATTGAATA TCCAGGAATT ATGAAAGACA  
 551 CTACAACCTA ACTGGATATA ACAGATTCTG AAGTGGAGAC TGCTCAAAAA  
 601 ATGGAATGA TTGAAGAAAC TGAAGCAGAT TCGACATTTG TAGGCGAGGA  
 651 TTCAAAGCT ACGAAACTG TGAGGACATC CAGTTCAAGT TTCCTGTCAA  
 701 CTGTTTCAAC ATGCGAAGCC CCTGCAAAAG GACGAGCAAG AATGTATCAA  
 751 AAAGAGTTGG AAAAGCATGT GATTGCATTT ACTGAGGGAA ATCTCACACT  
 801 ACAACGAGT TTGAACAAAG TTGATCCCGA CAGAACTAT CGATATTGTA  
 851 CAATTCCGAA CTTTCCAGCT TCCCAAGGAA AACTTCGAGA AGATAATCGA  
 901 TATGGCCCAA AAATCGTTTT GCCTCAAAGA TGGCGAGAAT TTGATTCGAG  
 951 GGGCCGTAGA AGAGACTCAT ATTTCTATTT CAAACGTAAG CTCGATGGAT



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1001 ATTTGAAATG CTACAAAACA ACTGGATATT TTATGTTTGT TGGACTTTTG
1051 CACAACATGT GGGAAATTTGA CCCAGACATC ACATATAAAC TGCCAGCACT
1101 GGAATGTAT TACAAAGAGA TGTCGGAATC TGTTGGTAGA GAAGAGGTTT
1151 TGGAAAAATT TGCACGAGTT GCCCGCATCG CAAAAACTGC TGAAGATATT
1201 TGCCAGAGC GAATTTATCG TCTTGTTGGT GACGTCGAAT CAGCTACCTT
1251 GAGCCACAAG CAATGTGCTG CACTTGTTGC GAGAATGTTT TTTGCCCCGAC
1301 CGGACAGTCC TTTCAGTTTC TGCCGAATTC TCTCGTCTGA TAAATCTATT
1351 TGTGTGGAGA AACTTAAATT CCTGTTCAC TATTTTCGACA AAATGTCAAT
1401 GGATCCACCG GATGGTGCCG TCAGTTTTAG ACTTACAAAA ATGGATAAAG
1451 ATACGTTCAA CGAAGAGTGG AAAGATAAAA AATTACGTTC TCTTCCTGAA
1501 GTTGAATTCT TTGATGAAAT GCTTATTGAA GACACAGCTC TCTGTACACA
1551 AGTTGATTTT GCGAACGAAC ATCTTGGTGG CGGAGTTTTA AATCATGGGT
1601 CTGTTCAAGG GGAGATCCGT TTCTTGATGT GTCCAGAAAT GATGGTTGGA
1651 ATGTTGTTGT GCGAGAAAAT GAAACAAC TGAGCGATTT CAATTGTTGG
1701 AGCTTACGTT TTCAGTTCCT ATACTGGTTA TGGTCATACT CTAAAAATGGG
1751 CAGAACTTCA ACCAAATCAT TCTCGTCAGA ATACAAACGA ATTTTCGAGAT
1801 CGTTTTGGAC GTCTTCGGGT AGAAACTATT GCAATCGATG CAATTCTGTT
1851 CAAAGGATCA AAATTAGATT GTCAGACGGA GCAGTTAAAC AAAGCAAATA
1901 TCATTAGGGA AATGAAGAAA GCATCTATCG GATTCATGAG CCAGGGACCG
1951 AAATTCACAA ATATTCCAAT TGTTACTGGA TGGTGGGGAT GTGGAGCATT
2001 TAATGGGGAC AAGCCACTGA AGTTCATAAT CCAAGTAATT GCTGCCGGAG
2051 TCGCTGATCG TCCACTTCAT TTCTGTTTAT TTGGAGAACC CGAGCTTGCC
2101 GCAAAGTGCA AGAAAATTAT AGAACGAATG AAACAGAAGG ACGTAACACT
2151 TGGTAAGTCA TGTTTTTCAA TCTTCAGTTG A

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(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 amino acids
- (B) TYPE: protein
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

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1 MSKKFIELDG PVTQDEKDYE DYVGVGFAHQ VPTMKRRKLT EHGNTTESKE DPEEPKSRDV
61 FVSSQSSDES QEDSAENPEI AKEVSENCEN LTETLKISNI ESLDNVTERS EHTLDNHKST
121 EPMEEDVNNK SNIDVAINSD EDDELVLEEN NKEMRDGEQV QQLSQDLFAD DQELIEYPGI
181 MKDTTTTQLDI TDSEVETAQK MEMIEETAD STFVGEDSKA TKTVRTSSSS FLSTVSTCEA
241 PAKGRARMYQ KELEKHVIAF TEGNLTLPD LNKVDPDRNY RYCTIPNFPA SQGKLREDNR
301 YGPKIVLPQR WREFDSRGRR RDSYFYFKRK LDGYLKCYKT TGYFMFVGLL HNMWEFDPDI
361 TYKLPALEMY YKEMSELVGR EEVLEKFARV ARIAKTAEDI LPERIYRLVG DVESATLSHK
421 QCAALVARMF FARPDSPFSF CRILSSDKSI CVEKLKFLFT YFDKMSMDPP DGAVSFRLTK
481 MDKDTFNEEW KDKKLRLSPE VEFFDEMLIE DTALCTQVDF ANEHLGGGVL NHGSVQEEIR
541 FLMCPEMMVG MLLCEKMKQL EASIVGAYV FSSYTGYGHT LKWAELOPNH SRQNTNEFRD
601 RFGRLRVETI AIDAILFKGS KLDCQTEQLN KANIIREMKK ASIGFMSQGP KFTNIPIVTG
661 WWGCGAFNGD KPLKFIIQVI AAGVADRPLH FCSFGEPELA AKCKKIIERM KQKDVTLGKS
721 CFSIFS

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(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: polypeptide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

LFTEVLHDNE CLIITGTEQY SEYTGyaety R

(2) INFORMATION FOR SEQ ID NO: 12:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 amino acids  
 (B) TYPE: polypeptide  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
  
 (ii) MOLECULE TYPE: protein fragment  
  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
AYCGFLRPGV SSENLSAVAT GNXGCGAFG

(2) INFORMATION FOR SEQ ID NO: 13:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 amino acids  
 (B) TYPE: polypeptide  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
  
 (ii) MOLECULE TYPE: protein fragment  
  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
FLINPELIVS R

(2) INFORMATION FOR SEQ ID NO: 14:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 16 amino acids  
 (B) TYPE: polypeptide  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
  
 (ii) MOLECULE TYPE: protein fragment  
  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
IALXLPNIXT QPIPLL

(2) INFORMATION FOR SEQ ID NO: 15:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 amino acids  
 (B) TYPE: polypeptide  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
  
 (ii) MOLECULE TYPE: protein fragment  
  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
GAYCAYAAYG ARTGYYT

(2) INFORMATION FOR SEQ ID NO: 16:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 amino acids  
 (B) TYPE: polypeptide  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
  
 (ii) MOLECULE TYPE: protein fragment  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
CKRTANGTYT CNGCRTA

- (2) INFORMATION FOR SEQ ID NO: 17:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 24 bases  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: oligonucleotide  
  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

ATCATCACAG GTACTGAGCA GTAC

- (2) INFORMATION FOR SEQ ID NO: 18:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 24 bases  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: oligonucleotide  
  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GCCTGTGTAT TCACTGTACT GCTC

- (2) INFORMATION FOR SEQ ID NO: 19:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 26 amino acids  
 (B) TYPE: polypeptide  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: polypeptide  
  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

EDKRKEQCEM KHRTERKIP KYIPPH

- (2) INFORMATION FOR SEQ ID NO: 20:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 26 amino acids  
 (B) TYPE: polypeptide  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: polypeptide  
  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

EDRRKEQWET KHRTERKIP KYVPPH

- (2) INFORMATION FOR SEQ ID NO: 21:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 26 amino acids  
 (B) TYPE: polypeptide  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: polypeptide  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

EDRRKEQCEV RHRTERKIP KYIPPN

- (2) INFORMATION FOR SEQ ID NO: 22:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 32 amino acids  
 (B) TYPE: polypeptide  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: polypeptide  
  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

HQVPTMKRRK LTEHGNTTES LLLKEDPPEP KS

- (2) INFORMATION FOR SEQ ID NO: 23:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 26 amino acids  
 (B) TYPE: polypeptide  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: polypeptide  
  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

EGKRKGDEVD GVDEVAKKKS KKEKDK

- (2) INFORMATION FOR SEQ ID NO: 24:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 26 amino acids  
 (B) TYPE: polypeptide  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: polypeptide  
  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

EGKRKGDEVD GTDEVAKKKS RKETDK

- (2) INFORMATION FOR SEQ ID NO: 25:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 26 amino acids  
 (B) TYPE: polypeptide  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: polypeptide  
  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

EGKRKGDEVD GIDEVTKKKS KKEKDK

- (2) INFORMATION FOR SEQ ID NO: 26:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 amino acids  
 (B) TYPE: polypeptide  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: polypeptide  
  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

EGKRKGEEVD GNVVAKKKS KEKEK

- (2) INFORMATION FOR SEQ ID NO: 27:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 26 amino acids
    - (B) TYPE: polypeptide
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: polypeptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

EGKRKADEV D GHSAATKKKI KKEKEK

- (2) INFORMATION FOR SEQ ID NO: 28:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 25 amino acids
    - (B) TYPE: polypeptide
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: polypeptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

EELPDTKR KAK MELSDTNEEG EKKQR

- (2) INFORMATION FOR SEQ ID NO: 29:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 31 amino acids
    - (B) TYPE: polypeptide
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: polypeptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

EGVSSAKKAK IEKIDEEDAA SIKELTEKIK K

- (2) INFORMATION FOR SEQ ID NO: 30:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 28 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: oligonucleotide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

GCTGCGGGTC TCGACGATGA GTGCGGGC

- (2) INFORMATION FOR SEQ ID NO: 31:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 29 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: oligonucleotide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

GCGTCTAGAA TTCACTTGGC TCCTCAGGC

- (2) INFORMATION FOR SEQ ID NO: 32:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 38 bases  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: oligonucleotide  
  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

CCGGAATTCG GGTTTTTTGT TAATGAAAAT TTATTAAC

- (2) INFORMATION FOR SEQ ID NO: 33:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 bases  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: oligonucleotide  
  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

TCAGAGCAGA TGAACGAG CAGTCCAGG

- (2) INFORMATION FOR SEQ ID NO: 34:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 61 bases  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: oligonucleotide  
  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

1 CCAATTTGAA GGAGGAATTC CCGCCGCCAC CATGAATGAT GTGAATGCCA AACGACCTGG  
61 A

- (2) INFORMATION FOR SEQ ID NO: 35:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 bases  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: oligonucleotide  
  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

gaattcccg cgcaccATG AA

- (2) INFORMATION FOR SEQ ID NO: 36:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 674 bases  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: cDNA  
  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```

1   agaagaaaat ggccaaggca tgctacaggt ggattttgca aatcgttttg ttggaggtgg
61  tgtaaccagt gcaggacttg tgcaagaaga aatccgcttt ttaatcaatc ctgagttgat
121 tatttcacgg ctcttcaactg aggtgctgga tcacaatgaa tgtctaatta tcacaggtac
181 tgagcagtac agtgaataca caggctatgc tgagacatat cgttggtccc ggagccacga
241 agatgggagt gaaagggacg actgcgagcg gcgctgcaact gagatcgttg ccatcgatgc
301 tcttcaacttc agacgctacc tcgatcagtt tgtgcctgag aaaatgagac gcgagctgaa
361 caaggcttac tgtggatttc tccgtcctgg agtttcttca gagaatcttt ctgcagtggc
421 cacaggaaac tggggctgtg gtgcctttgg gggatgatgcc aggttaaaag ccttaataca
481 gatattggca gctgctgcag ctgagcgaga tgtggtttat ttcacctttg gggactcaga
541 attgatgaga gacatttaca gcatgcacat tttccttact gaaaggaaac tcaactgttg
601 agatgtgtat aagctgttgc tacgatacta caatgaagaa tgcagaaact gttccacccc
661 tggaccagac atca

```

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

```

1   aaaaatagtt gtcaagactc agaagcagat gaggagacaa gtccaggttt tgatgaacaa
61  gaagatggta gttcctccca aacagcaaat aaaccttcaa ggttccaagc aagagacgct
121 gacattgaat ttaggaaacg gtactctact aaggcggtg aagttagatt acatttccaa
181 tttgaaggag gagagagtcg

```

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```

1   gatctcgaag taaaaactca cgcagaaaga gtcctcctc ctttagcatg agaatccaac
61  tttgtaatga taacactggc aacatcaaca gtttgagaga aagcacgtgc ttgggcttca
121 caagcttgct caatagaagc atccatcaca aaaacaacat tatctggtgt aactgcgttg
181 gaaacttgga gcatttcttc gaaaagtga gcttcttgct tgtgacgacc tgatgtatca
241 acaatgatga tttcgaaccc ttcttgctgc aaaacaaata ttattaaacc atttttctgt
301 gataaattac cgtgaatttt tctactcctt cggcgccaat ttttacgggg tcaatttcag
361 agtatgatcc atagaaggga atacgagctt ttgtggcatt ttgctttaat tgatcaaaag
421 ctccagcacg gaatgtatcg gcacagatca gacatgtttt ccattccttt ctttggtagt
481 aatacgccat ctgaacttga aaagtgttga aaagtgttg gaagtttact aattaaaaaa
541 tataatgttt gatggtgtgt gagctttcta ttgtaattca tggaacgaac cttggtacaa
601 gtcgtagttt taccggaacc ttgaagacca acaaacatga aaacgttgcg acgtcctttt
661 gttggtgtga aaggagttac accaggatcc acaagcttca gcagttcatt gaatactgtc
721 ttctgaatgt accgacgttt gtttgcctct ccgacgatct cttcgaaatt aatcgctttt
781 ctgaaaatat ttattaaatt taaatcttaa atagcgtaaa aatttacttc acgttgctct
841 taagttgctt tacaagacga atatgaacat cagattcaat aagagctgta cagacttctt
901 tcagcatcaa atccagctcc cctcatttga taacggtgct ctgaccgagc tttccgatcg
961 catttcggat tttccgcccc aaatcgcca aaaccatttt gaactgaaat ttgaaatgct
1021 ttaatttggt taagcataga attaaacgcg ttttaaatac agagcaccat aaaaacagtt
1081 tggagaaaaa tcgataattc ttgtaggaga ttcagtcctt gtggttttct tcggtcttct
1141 aatcattttt tgacgacata gtggtatttc acaataggtt ttttcaagac acaacagatt
1201 tttcacaaag agtagagaag aaatggaaaa ctgtagattt cttctcgaag agccgagaaa
1261 ggcaagggtat tggaagttaa aaaaggtaat gtttctttat tcttttttca aaacaataat

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1321	aaatggaaaa	tatatatttta	tagataacaa	tttcagacag	ttaaaatcac	gtgaaaaatt
1381	caaattttcaa	cacaaaaaatt	gacgagtggga	accccgttgt	tgcgcccttga	agagtaacgc
1441	ttgcgcggttt	gacgattttta	ttgacgcggtt	tctggtgcat	gcgggaaaatt	ttttatttttc
1501	aactttttttc	ctgttttggtt	atccttttttt	aattgaatttc	tcatgatttg	aaagcctttga
1561	aaaatatttat	tttgctcaaaa	aacatgcggtt	ttgtaaaaaca	ttgatttagat	tcaaggcaat
1621	taatggatttt	ttgcacggttc	caaaaaaaaag	gaaattcatt	ttttgaaaat	tttgataaatt
1681	taataatgaa	aaatgttcca	tagattttatt	caatgccatc	cttctctata	atctcgaact
1741	tccgcacacct	tcaactgtgg	tagaggtatt	tgcaataacca	tatagtcgta	ataataaact
1801	ttagtgaaca	aatccaagac	atcagctctt	gagtaaataga	atgattttata	aaaactgctg
1861	attttctcgt	aggaagaaaag	agaatcagct	aataatccgt	cgttgtctat	ctgtcaggc
1921	cgctttaaattg	ttaaaaaata	aaaacgttttt	aagctaatttt	tgtatgtcta	gaaactctaa
1981	ctcacaagca	tttctgcata	cgccggatta	gttgggttttg	caaaaagcga	gtaatctaca
2041	aaagtgaatt	tttgattcat	ctcttccatt	tcacaaaacc	aattttgtgg	tacgtatttc
2101	atatgatctt	catccacttt	tttagttttt	gaatgtattt	gtgtgagttg	tgtccagatt
2161	tgaataagat	aacatctcag	atccaacttg	caattgaagc	aagaacgatc	ttctctgaaa
2221	ttttatatga	ccttaaaact	tagtttcttg	tagtttctgc	gatatctgat	cgttcagttg
2281	ttaggtatg	tacatctcta	ggtttatgtg	ctacacgaaa	atataatttg	ttttacctaa
2341	cacacgcac	cataaaatga	tctacaaatc	gttcaattgg	atcctgtctt	ggaaataata
2401	atttccaatt	cgtaaagttt	gcattcaact	cattttctcg	tttcaaatcg	tcgatatccg
2461	caaaatatgt	tagtgaatca	ctatcacaca	ctctgaaaag	cacaatatc	atatttcgta
2521	gttaataatg	aacctcacga	ttcatcatta	aattttctct	ggagcccgcga	taataactgc
2581	tgcccaatta	aagtatcag	ttcacagatt	gcagttctat	catttccgat	agcctcaaat
2641	aagattttaat	cttaagcgag	tgttctgatac	aattttaaata	tttgatactc	accgcaagtt
2701	tcttcgaaac	ttgttcgaaa	gctggaattt	tagaatatcc	ttcaaaactt	ttttcctcgc
2761	cctcatcaag	ccataataag	ttttgatcag	caatatattc	gaataaatta	gtctctgata
2821	aatctcgtat	cacaatcttt	ttttctactc	taaagaatac	aattttgata	agaatgataa
2881	taattataat	tataatagtt	cgctcgtgag	ttgatgaaga	ccacataatt	agtttaattg
2941	caagctatgc	aacttgttga	atactaatag	gacttagcaa	atcttatctt	gaaccttttt
3001	cattcgaag	aaaaatgaga	tcgaatctcg	ttcaaaactgt	ggagtagtca	gttaagaaac
3061	ttgtttctag	tttgtgagga	gacactggag	aacgtgaaaag	tattacccat	acgcaatatt
3121	tttgccggcga	aaaatacggg	acccggtctc	gacacgacag	tttttaaaac	ttgtaaatag
3181	gtatgtaaaa	gaaaacttta	attttaaacg	tgttgtttcg	gaattttcat	cgttttgtca
3241	tagttattct	acaaataatt	atttatgaaa	aaaaaactaa	aatataacta	taataacacc
3301	tgaattattaa	caaatcgatc	gaaaaaaaac	tatgaaaaaa	atggatgaaa	attccgcagc
3361	aacgagaggt	tgaaatttca	gtattcttta	aaggcttacc	gatttcaata	aatagtgaca
3421	ctgaaaattg	tagtttttaa	actagttggg	tagtatcatc	aaatattcaa	tccttcaaaa
3481	attcctcaat	attaacgtat	tttctctaatt	tgtcttcatt	atctaaaaaa	aagttgcaat
3541	atattttttcc	aggcagaaat	agactttcac	aaaacacatc	gacacttcga	atgagcaaga
3601	agttttatoga	actgggtgat	cctgtcactc	aagacgttag	ttatagtttt	tattacttga
3661	acattatcat	cttttttacag	gagaaagact	acgaagacta	tgtcggaggt	ggtttcgcgc
3721	atcaagtccc	gacaatgaaa	aggcggaagt	tgacagaaca	tggaataact	acagaatcaa
3781	aagaagatcc	tgaagagcca	aaaagccgtg	acgtatttgt	ctcctcgcag	tcaagtgatg
3841	agagtcaaga	agattcggct	gaaaatccgg	agatcgctaa	agaagtgtca	gaaaatttgt
3901	aaaatctgac	agaaactctc	aaaatttcta	atattgagag	tttgacaat	gttactgaaa
3961	gatctgaaca	cactcttgat	aatcacaaaa	gtactgaacc	aatggaagaa	gatgtaaaca
4021	acaagtccaa	tattgacgtt	gcgattaatt	ctgacgagga	tgatgaactt	ggtctggaag
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4141	gaatgaaata	agttaatcac	caaaatgaat	aaggacattt	cccatcagaa	aggtcttctg
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4261	aaaatttagtt	attgcatacc	cttcatgttt	ttgaagattg	tttaggaatg	agaaaacatt
4321	ttggacgctt	ttattattag	gacaccaaac	actttttgtt	gaaaaaacag	ctcgtttaaa
4381	aaaagctttt	tccaaaaaat	ctgacgcaag	gcttgtgaat	tttctgtttt	ccctgatttt
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4621	gatgccgggt	accttatttt	tggttcaaaa	atcccaatat	tacgcgtctg	ggttatagtc
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5041	tccaaaaata	ataatgtact	gcagttgtca	caggatttat	tcgctgatga	tcaagagcta
5101	attgaatatc	caggaattat	gaaagacact	acaactcaac	tggatataac	agattctgaa
5161	gtggagactg	ctcaaaaaat	ggaaatgatt	gaagaaactg	aagcagattc	gacatttgta
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6181	atataatttaa	ttattttcaga	acttcgagaa	gataatcgat	atggcccaaa	aatcgttttg
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6541	gttgaaaatc	atgtttttcaa	aagatgcatt	ttttattcct	tctcgatttt	ttttgatttt
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6661	actcaaaaatt	ttctgaaaaa	gccaaaattt	ataatgaaac	ttcttgaaaa	ctcttcagca
6721	aaaagtattg	acggctcaaa	aaatggccta	aaattagtta	agattggaga	tttgaccgac
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6961	aagaataaaa	caaaaggtag	gcaacttgta	tattcaaaaat	ttgacgggtg	ttgcaacttt
7021	taactaattt	caggccattt	tttgagccgt	cataactttt	ttctaaaaag	ttttcaagaa
7081	gtttcattat	gaaattcggg	gttttcagac	aaattttgagt	ctaataagga	aataaaaaaaa
7141	attcaggtac	accaccttta	agaaaatttt	ggatttccgc	tacgctaata	cacctttaat
7201	caaaaaatatt	tgaagttatt	caaagttaaa	gaatttatatt	ttcagagggg	ccgtagaaga
7261	gactcatatt	tctatlttcaa	acgtaagctc	gatggatatt	tgaatgcta	caaaaacaact
7321	ggatattttta	tgltttgttgt	aagtttttga	aatacaattc	gtttgaagat	ttactctatt
7381	ttcagggact	tttgacacaac	atgtgggaat	ttgacccaga	catcacatat	aaactgccag
7441	cactggaaat	gtattacaaa	gagatgtcgg	aaactgttgg	tagagaagag	gttttggaaa
7501	aatlttgacg	agttgcccgc	atcgcaaaaa	ctgctgaaga	tattctgccca	gagggtatgat
7561	ttatgagata	tacagcattt	cctctaatag	tattgcatat	aaacatttca	ctttgaggtt
7621	atatcttggt	ttatltttaaa	aatatcaata	aatacaaaaac	aatagaaaaa	tgataaaaaa
7681	acattttgtc	agttgataat	ttgggtatag	tattcattca	taattttgatt	tttttagcga
7741	atlttatcgtc	ttgttggtga	cgtcgaatca	gctacettga	gccacaagca	atgtgctgca
7801	cttggtgcga	gaatgttttt	tgcccagccg	gacagtcctt	tcagtttctg	ccggtgagta
7861	atacaagaat	gctcatattt	ttagaatcaa	tatttgcaag	gaactttaat	cttactgtacg
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7981	agcttctgta	actcgtatca	atlttacaagc	cgttattaca	tcagttttta	atgaattttta
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